

Hum: 1 MATAGGSGADPGSRGLRLLSFCVLLAGLCRGNVSVERKIYIPLNKTA PCVRLLNATHQI 60
Mou MAT GSGG DPGSRGL LLSF V+LAGLC GNSVERKIYIPLNKTA PCVRLLNATHQI
Dros: 1 A + +G K+Y P+ A C R LN THQ
C.ele L +++AG+C G S + + + C R N TH+

Hum 61 GCQSSISGDTGVIHVEKEEDLQWVLTGDPNPPYMWLLESKHFTTRDIMKLGKRTSRIAG 120
Mou GCQSSISGDTGVIHVEKEEDL+WVLTGDPNPPYMWLLE K FTRD+MEKLG TSRIAG
Dros GC S+ SG GV+H++ E DL+++L+ P+PPY ++ FTR+ + +LK +
C.eleg GCQ++ + G+I ++K+ED + W + Y LL RD + +LK + ++G

Hum: 121 LAVSLTKPSPASGSPSVQCPNDGFGVYSNSYGPFAHCREIQWNSLGNGLAYEDFSFPI 180
Mou LAV+L KP+ S FSPSVQCPNDGFG YSNSYGPFAH ++ WN LG GLAYED SFPI
Dros + + + + FS + CPN G+ S S + ++ + WN G GL +EDF FPI
C.eleg + +S + ++ S +CPN Y E+ E + NS G+GL D+ +

Hum: 181 FLEEDENETKVIKQCYQDHNLSQNGSAPTFLCAMQLFSHMAVISTATCMRRSSIQSTF 240
Mou FLEDE+ETKVIKQCYQDHNL QNGSAP+FPLCAMQLFSHMAVISTATCMRRS IQSTF
Dros : + + D ++ ++C+QD N + LCA+++ S M A ++T CMRR++ +
C.eleg +++ + ++I++CY N + + +P C M A ++ C RR + F

Hum: 241 SINPEIVCDPLSDYNWWSMLKPINTTGLKPPDRVVVAATRLDSRSFF-WNVAPGAESAV 299
Mous SINPEIVCDPLSDYNWWSMLKPINT+ L+PD RVVVAATRLDSRSFF WNVAPG ESAV
Dros ++ CDPL NV P +T T+ +++ ++ RLD+ + F V GA ++
C.eleg +N + +C + N+++ PI T+ T+ + ++ R+DS ++ G S +

Hum: 300 ASFVTQLAAAEALQKAPDVTTLLPRNMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENV 359
Mou ASFVTQLAAAEAL KAPDVTTLL.RNMFVFFQGETFDYIGSSRMVYDME KGKFPV+LEN+
Dros F A LQ P + NV+FV F GE++DYIGS R VYDMEK +Fp+ +N+
C.eleg S ++ LAAA ++/QKA + + RNV F FF GE+ DYIGS Y ME GKFP++ +

Figure 1A

Figure 1B